

Eduan Wilkinson

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

39
papers

2,048
citations

18
h-index

43
g-index

43
ext. papers

3,870
ext. citations

16.1
avg, IF

4.87
L-index

#	Paper	IF	Citations
39	Detection of a SARS-CoV-2 variant of concern in South Africa. <i>Nature</i> , 2021 , 592, 438-443	50.4	685
38	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma. <i>Nature</i> , 2021 , 593, 142-146	50.4	344
37	Sixteen novel lineages of SARS-CoV-2 in South Africa. <i>Nature Medicine</i> , 2021 , 27, 440-446	50.5	206
36	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa.. <i>Nature</i> , 2022 ,	50.4	205
35	Escape of SARS-CoV-2 501Y.V2 from neutralization by convalescent plasma		71
34	The emergence and ongoing convergent evolution of the SARS-CoV-2 N501Y lineages. <i>Cell</i> , 2021 , 184, 5189-5200.e7	56.2	61
33	Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation during a Pandemic. <i>Genes</i> , 2020 , 11,	4.2	39
32	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report. <i>International Journal of Infectious Diseases</i> , 2021 , 103, 234-241	10.5	37
31	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021 , 374, 423-431	33.3	35
30	Persistent SARS-CoV-2 infection and intra-host evolution in association with advanced HIV infection		32
29	A genomics network established to respond rapidly to public health threats in South Africa. <i>Lancet Microbe, The</i> , 2020 , 1, e229-e230	22.2	30
28	Identifying Recent HIV Infections: From Serological Assays to Genomics. <i>Viruses</i> , 2015 , 7, 5508-24	6.2	23
27	Emergence and phenotypic characterization of C.1.2, a globally detected lineage that rapidly accumulated mutations of concern		23
26	Origin, imports and exports of HIV-1 subtype C in South Africa: A historical perspective. <i>Infection, Genetics and Evolution</i> , 2016 , 46, 200-208	4.5	22
25	SARS-CoV-2 prolonged infection during advanced HIV disease evolves extensive immune escape.. <i>Cell Host and Microbe</i> , 2022 ,	23.4	22
24	Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report 2020 ,		20
23	HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens. <i>Cell Host and Microbe</i> , 2021 , 29, 1093-1110	23.4	19

22	History and origin of the HIV-1 subtype C epidemic in South Africa and the greater southern African region. <i>Scientific Reports</i> , 2015 , 5, 16897	4.9	18
21	A novel variant of interest of SARS-CoV-2 with multiple spike mutations detected through travel surveillance in Africa		17
20	High Resolution analysis of Transmission Dynamics of Sars-Cov-2 in Two Major Hospital Outbreaks in South Africa Leveraging Intra-host Diversity 2020 ,		15
19	Tracking external introductions of HIV using phylodynamics reveals a major source of infections in rural KwaZulu-Natal, South Africa. <i>Virus Evolution</i> , 2018 , 4, vey037	3.7	15
18	SARS-CoV-2 shifting transmission dynamics and hidden reservoirs potentially limit efficacy of public health interventions in Italy. <i>Communications Biology</i> , 2021 , 4, 489	6.7	13
17	Rapid epidemic expansion of the SARS-CoV-2 Omicron variant in southern Africa		12
16	SARS-CoV-2 evolved during advanced HIV disease immunosuppression has Beta-like escape of vaccine and Delta infection elicited immunity. 2021 ,		12
15	Next Generation Sequencing and Bioinformatics Analysis of Family Genetic Inheritance. <i>Frontiers in Genetics</i> , 2020 , 11, 544162	4.5	11
14	Analysis of Viral Diversity in Relation to the Recency of HIV-1C Infection in Botswana. <i>PLoS ONE</i> , 2016 , 11, e0160649	3.7	9
13	Multiple Early Introductions of SARS-CoV-2 to Cape Town, South Africa. <i>Viruses</i> , 2021 , 13,	6.2	9
12	Detection of transmission clusters of HIV-1 subtype C over a 21-year period in Cape Town, South Africa. <i>PLoS ONE</i> , 2014 , 9, e109296	3.7	8
11	Sequencing and phylogenetic analysis of near full-length HIV-1 subtypes A, B, G and unique recombinant AC and AD viral strains identified in South Africa. <i>AIDS Research and Human Retroviruses</i> , 2015 , 31, 412-20	1.6	7
10	Combining Phylogenetic and Network Approaches to Identify HIV-1 Transmission Links in San Mateo County, California. <i>Frontiers in Microbiology</i> , 2018 , 9, 2799	5.7	5
9	SARS-CoV-2 Genetic diversity and lineage dynamics of in Egypt		3
8	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa		3
7	Emergence and phenotypic characterization of the global SARS-CoV-2 C.1.2 lineage.. <i>Nature Communications</i> , 2022 , 13, 1976	17.4	3
6	High rate of occult hepatitis B virus infection in hemodialysis units of KwaZulu-Natal, South Africa. <i>Journal of Medical Virology</i> , 2019 , 91, 1797-1803	19.7	2
5	Factors influencing HIV-1 phylogenetic clustering. <i>Current Opinion in HIV and AIDS</i> , 2019 , 14, 161-172	4.2	2

4	Comparison of SARS-CoV-2 sequencing using the ONT GridION and the Illumina MiSeq.. <i>BMC Genomics</i> , 2022 , 23, 319	4.5	2
3	Replacement of the Gamma by the Delta variant in Brazil: Impact of lineage displacement on the ongoing pandemic.. <i>Virus Evolution</i> , 2022 , 8, veac024	3.7	1
2	The role of high-risk geographies in the perpetuation of the HIV epidemic in rural South Africa: A spatial molecular epidemiology study. <i>PLOS Global Public Health</i> , 2022 , 2, e0000105		0
1	The geography and inter-community configuration of new sexual partnership formation in a rural South African population over fourteen years (2003–2016). <i>PLOS Global Public Health</i> , 2022 , 2, e0000055		